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1108

#2

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,421

DATE: 11/02/2001

TIME: 15:08:38

Input Set : A:\3086-A SeqListce filed 101701.txt

Output Set: N:\CRF3\11022001\I981421.raw

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3 <110> APPLICANT: Sims, John E.
4      Mohler, Kendall M.
5      Born, Teresa L.
7 <120> TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEDIATED DISORDERS
9 <130> FILE REFERENCE: 3086-A
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/981,421
12 <141> CURRENT FILING DATE: 2001-10-17
14 <150> PRIOR APPLICATION NUMBER: US 60/241,408
15 <151> PRIOR FILING DATE: 2000-10-18
17 <160> NUMBER OF SEQ ID NOS: 5
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2681
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (484)..(2283)
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37 ttatgtctta agagcaggaa ataaagagac agctgaaggt gtagccttga ccaactgaaa      180
39 gggaaatctt catcctctga aaaaacatat gtgattctca aaaaacgcat ctggaaaatt      240
41 gataaagaag cgattctgta gattctccca gcgctgttgg gctctcaatt ccttctgtga      300
43 aggacaacat atggtgatgg ggaaatcaga agctttgaga cctctacac ctggatatga      360
45 atcccccttc taatacttac cagaaatgaa ggggatactc agggcagagt tctgaatctc      420
47 aaaacactct actctggcaa aggaatgaag ttattggagt gatgacagga acacgggaga      480
49 aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag      528
50      Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu
51      1          5          10          15
53 cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt      576
54 Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu
55      20          25          30
57 tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat      624
58 Trp Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp
59      35          40          45
61 tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca      672
62 Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser
63      50          55          60
65 cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta      720
66 Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu
67      65          70          75
69 tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag      768
70 Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu
71 80          85          90          95
73 gac att agg aaa agc tat cct cac atc att cag gac aaa tgt acc ctt      816

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78 His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg
79          115          120          125
81 ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg      912
82 Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met
83          130          135          140
85 att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca      960
86 Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala
87          145          150          155
89 tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc      1008
90 Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys
91 160          165          170          175
93 ccc agt ctc agc tgc caa agt gat gca caa agt cca gcg gta acc tgg      1056
94 Pro Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp
95          180          185          190
97 tac aag aat gga aaa ctc ctc tct gtg gaa agg agc aac cga atc gta      1104
98 Tyr Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val
99          195          200          205
101 gtg gat gaa gtt tat gac tat cac cag ggc aca tat gta tgt gat tac      1152
102 Val Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr
103          210          215          220
105 act cag tcg gat act gtg agt tcg tgg aca gtc aga gct gtt gtt caa      1200
106 Thr Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln
107          225          230          235
109 gtg aga acc att gtg gga gac act aaa ctc aaa cca gat att ctg gat      1248
110 Val Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp
111 240          245          250          255
113 cct gtc gag gac aca ctg gaa gta gaa ctt gga aag cct tta act att      1296
114 Pro Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile
115          260          265          270
117 agc tgc aaa gca cga ttt ggc ttt gaa agg gtc ttt aac cct gtc ata      1344
118 Ser Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile
119          275          280          285
121 aaa tgg tac atc aaa gat tct gac cta gag tgg gaa gtc tca gta cct      1392
122 Lys Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro
123          290          295          300
125 gag gcg aaa agt att aaa tcc act tta aag gat gaa atc att gag cgt      1440
126 Glu Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg
127          305          310          315
129 aat atc atc ttg gaa aaa gtc act cag cgt gat ctt cgc agg aag ttt      1488
130 Asn Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe
131 320          325          330          335
133 gtt tgc ttt gtc cag aac tcc att gga aac aca acc cag tcc gtc caa      1536
134 Val Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln
135          340          345          350
137 ctg aaa gaa aag aga gga gtg gtg ctc ctg tac atc ctg ctt ggc acc      1584
138 Leu Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr

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142	Ile Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg							
143		370		375		380		
145	cac tgg att gaa ata gtg ctg ctg tac cgg acc tac cag agc aag gat							1680
146	His Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp							
147		385		390		395		
149	cag acg ctt ggg gat aaa aag gat ttt gat gct ttc gta tcc tat gca							1728
150	Gln Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala							
151	400		405		410		415	
153	aaa tgg agc tct ttt cca agt gag gcc act tca tct ctg agt gaa gaa							1776
154	Lys Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu							
155		420		425		430		
157	cac ttg gcc ctg agc cta ttt cct gat gtt tta gaa aac aaa tat gga							1824
158	His Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly							
159		435		440		445		
161	tat agc ctg tgt ttg ctt gaa aga gat gtg gct cca gga gga gtg tat							1872
162	Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr							
163		450		455		460		
165	gca gaa gac att gtg agc att att aag aga agc aga aga gga ata ttt							1920
166	Ala Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe							
167		465		470		475		
169	atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa							1968
170	Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln							
171	480		485		490		495	
173	gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta							2016
174	Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu							
175		500		505		510		
177	att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg							2064
178	Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val							
179		515		520		525		
181	aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa							2112
182	Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys							
183		530		535		540		
185	tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg							2160
186	Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met							
187		545		550		555		
189	cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc							2208
190	Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr							
191	560		565		570		575	
193	tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg							2256
194	Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly							
195		580		585		590		
197	agg agc tcc cag cct aag gaa tgg tga aatgagccct ggagccccct							2303
198	Arg Ser Ser Gln Pro Lys Glu Trp							
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201	ccagtccagt ccctgggata gagatgttgc tggacagaac tcacagctct gtgtgtgtgt							2363
203	gttcaggctg ataggaaatt caaagagtct cctgccagca ccaagcaagc ttgatggaca							2423
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218 <212> TYPE: PRT
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228 20 25 30
231 Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp Leu
232 35 40 45
235 Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro
236 50 55 60
239 Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser
240 65 70 75 80
243 Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp
244 85 90 95
247 Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His
248 100 105 110
251 Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro
252 115 120 125
255 Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile
256 130 135 140
259 Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser
260 145 150 155 160
263 His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro
264 165 170 175
267 Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr
268 180 185 190
271 Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val
272 195 200 205
275 Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr
276 210 215 220
279 Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val
280 225 230 235 240
283 Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro
284 245 250 255
287 Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser
288 260 265 270
291 Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys
292 275 280 285
295 Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu
296 290 295 300
299 Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn
300 305 310 315 320

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307 Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu
308                               340                      345          350
311 Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile
312                               355                      360          365
315 Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His
316                               370                      375          380
319 Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln
320 385                               390                      395          400
323 Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys
324                               405                      410          415
327 Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His
328                               420                      425          430
331 Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr
332                               435                      440          445
335 Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala
336                               450                      455          460
339 Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile
340 465                               470                      475          480
343 Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala
344                               485                      490          495
347 Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile
348                               500                      505          510
351 Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys
352                               515                      520          525
355 Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser
356                               530                      535          540
359 Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro
360 545                               550                      555          560
363 Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser
364                               565                      570          575
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372                               595
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378 <213> ORGANISM: Homo sapiens
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,421

DATE: 11/02/2001

TIME: 15:08:39

Input Set : A:\3086-A SeqListce filed 101701.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number